



SEQUENCE LISTING

<110> KUSTERS, Johannes G.
CATTOLI, Giovanni

<120> HELICOBACTER FELIS VACCINES

<130> KUSTERS

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<141> 2001-07-13

<150> EP00202565.8

<151> 2000-07-17

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<170> PatentIn Ver. 2.1

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Lys Phe Leu Leu Tyr Tyr Ala Gly Glu Val Ala Arg Lys Arg Lys Ala

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Val Gly Asn Met Val Pro Asp Leu Gly Val Glu Ala Thr Phe Pro Asp	
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Gly Thr Lys Leu Val Thr Val Asn Trp Pro Ile Glu Pro Asp Glu His	
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Gln Leu Ile Pro Leu Gly Gly Ser Lys Lys Val Ile Gly Met Asn Gly	
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Leu Val Asn Asn Ile Ala Asp Glu Arg His Lys His Lys Ala Leu Asp	
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165 170 175
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Pro Glu Ala Ile Ala Tyr Ile Ser Ala His Ile Met Asp Glu Ala Arg
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Arg Gly Lys Lys Thr Val Ala Glu Leu Met Glu Glu Cys Met His Phe
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Glu Leu Glu Val Thr Asn Glu Gly Pro Lys Ser Leu His Val Gly Ser
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 750 755 760 765

cct aaa acc ttc gag gtc ttt gta gat ggc aaa ctc tgc acc tct aaa 2353
 Pro Lys Thr Phe Glu Val Phe Val Asp Gly Lys Leu Cys Thr Ser Lys
 770 775 780

ccc gcc tct gaa gtg cct cta gcc caa cgc tac act ttc ttc tag 2398
 Pro Ala Ser Glu Val Pro Leu Ala Gln Arg Tyr Thr Phe Phe
 785 790 795

gcacaat 2405

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 <211> 226
 <212> PRT
 <213> Helicobacter felis

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 Gly Glu Val Ala Arg Lys Arg Lys Ala Glu Gly Leu Lys Leu Asn Gln
 20 25 30
 Pro Glu Ala Ile Ala Tyr Ile Ser Ala His Ile Met Asp Glu Ala Arg
 35 40 45
 Arg Gly Lys Lys Thr Val Ala Glu Leu Met Glu Glu Cys Met His Phe
 50 55 60
 Leu Lys Lys Asp Glu Val Met Pro Gly Val Gly Asn Met Val Pro Asp
 65 70 75 80
 Leu Gly Val Glu Ala Thr Phe Pro Asp Gly Thr Lys Leu Val Thr Val
 85 90 95
 Asn Trp Pro Ile Glu Pro Asp Glu His Phe Lys Ala Gly Glu Val Lys
 100 105 110
 Phe Gly Cys Asp Lys Asp Ile Glu Leu Asn Ala Gly Lys Glu Val Thr
 115 120 125
 Glu Leu Glu Val Thr Asn Glu Gly Pro Lys Ser Leu His Val Gly Ser
 130 135 140
 His Phe His Phe Phe Glu Thr Asn Lys Ala Leu Lys Phe Asp Arg Glu
 145 150 155 160
 Lys Ala Tyr Gly Lys Arg Leu Asp Ile Pro Ser Gly Asn Thr Leu Arg
 165 170 175
 Ile Gly Ala Gly Gln Thr Arg Lys Val Gln Leu Ile Pro Leu Gly Gly
 180 185 190
 Ser Lys Lys Val Ile Gly Met Asn Gly Leu Val Asn Asn Ile Ala Asp
 195 200 205
 Glu Arg His Lys His Lys Ala Leu Asp Lys Ala Lys Ser His Gly Phe
 210 215 220

Ile Lys
225

<210> 6
<211> 568
<212> PRT
<213> *Helicobacter felis*

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Gly Asp Lys Val Arg Leu Gly Asp Thr Asp Leu Trp Ala Glu Val Glu
20 25 30
His Asp Tyr Thr Thr Tyr Gly Glu Leu Lys Phe Gly Ala Gly Lys
35 40 45
Thr Ile Arg Glu Gly Met Gly Gln Ser Asn Ser Pro Asp Glu Asn Thr
50 55 60
Leu Asp Leu Val Ile Thr Asn Ala Met Ile Ile Asp Tyr Thr Gly Ile
65 70 75 80
Tyr Lys Ala Asp Ile Gly Ile Lys Asn Gly Lys Ile His Gly Ile Gly
85 90 95
Lys Ala Gly Asn Lys Asp Met Gln Asp Gly Val Ser Pro His Met Val
100 105 110
Val Gly Val Gly Thr Glu Ala Leu Ala Gly Glu Gly Met Ile Ile Thr
115 120 125
Ala Gly Gly Ile Asp Ser His Thr His Phe Leu Ser Pro Gln Gln Phe
130 135 140
Pro Thr Ala Leu Ala Asn Gly Val Thr Thr Met Phe Gly Gly Gly Thr
145 150 155 160
Gly Pro Val Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro Gly Lys Trp
165 170 175
Asn Leu His Arg Met Leu Arg Ala Ala Glu Glu Tyr Ser Met Asn Val
180 185 190
Gly Phe Leu Gly Lys Gly Asn Ser Ser Ser Lys Lys Gln Leu Val Glu
195 200 205
Gln Val Glu Ala Gly Ala Ile Gly Phe Lys Leu His Glu Asp Trp Gly
210 215 220
Thr Thr Pro Ser Ala Ile Asp His Cys Leu Ser Val Ala Asp Glu Tyr
225 230 235 240
Asp Val Gln Val Cys Ile His Thr Asp Thr Val Asn Glu Ala Gly Tyr
245 250 255
Val Asp Asp Thr Leu Asn Ala Met Asn Gly Arg Ala Ile His Ala Tyr
260 265 270
His Ile Glu Gly Ala Gly Gly Gly His Ser Pro Asp Val Ile Thr Met
275 280 285
Ala Gly Glu Leu Asn Ile Leu Pro Ser Ser Thr Thr Pro Thr Ile Pro
290 295 300

Tyr Thr Ile Asn Thr Val Ala Glu His Leu Asp Met Leu Met Thr Cys
 305 310 315 320
 His His Leu Asp Lys Arg Ile Arg Glu Asp Leu Gln Phe Ser Gln Ser
 325 330 335
 Arg Ile Arg Pro Gly Ser Ile Ala Ala Glu Asp Val Leu His Asp Ile
 340 345 350
 Gly Val Ile Ala Met Thr Ser Ser Asp Ser Gln Ala Met Gly Arg Ala
 355 360 365
 Gly Glu Val Ile Pro Arg Thr Trp Gln Thr Ala Asp Lys Asn Lys Lys
 370 375 380
 Glu Phe Gly Lys Leu Pro Glu Asp Gly Ala Asp Asn Asp Asn Phe Arg
 385 390 395 400
 Ile Lys Arg Tyr Ile Ser Lys Tyr Thr Ile Asn Pro Ala Leu Thr His
 405 410 415
 Gly Val Ser Glu Tyr Ile Gly Ser Val Glu Glu Gly Lys Ile Ala Asp
 420 425 430
 Leu Val Val Trp Asn Pro Ala Phe Phe Gly Val Lys Pro Lys Ile Val
 435 440 445
 Ile Lys Gly Gly Met Val Val Phe Ser Glu Met Gly Asp Ser Asn Ala
 450 455 460
 Ser Val Pro Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met Phe Gly His
 465 470 475 480
 His Gly Lys Ala Lys Phe Asp Thr Ser Ile Thr Phe Val Ser Lys Val
 485 490 495
 Ala Tyr Glu Asn Gly Val Lys Glu Lys Leu Gly Leu Glu Arg Lys Val
 500 505 510
 Leu Pro Val Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp Phe Lys Phe
 515 520 525
 Asn Asn Lys Thr Ala His Ile Thr Val Asp Pro Lys Thr Phe Glu Val
 530 535 540
 Phe Val Asp Gly Lys Leu Cys Thr Ser Lys Pro Ala Ser Glu Val Pro
 545 550 555 560
 Leu Ala Gln Arg Tyr Thr Phe Phe
 565

<210> 7
 <211> 2183
 <212> DNA
 <213> Helicobacter felis

<220>
 <221> CDS
 <222> (3)..(683)

<220>
 <221> CDS

<222> (694)..(2181)

<400> 7

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	1				5					10					15	
gcg	ggc	gaa	gtg	gct	aga	aag	cgc	aaa	gca	gag	ggc	tta	aag	ctc	aat	95
	Ala	Gly	Glu	Val	Ala	Arg	Lys	Arg	Lys	Ala	Glu	Gly	Leu	Lys	Leu	Asn
				20					25					30		
caa	ccc	gaa	gcc	att	gcc	tac	att	agt	gcc	cat	att	atg	gac	gag	gcg	143
	Gln	Pro	Glu	Ala	Ile	Ala	Tyr	Ile	Ser	Ala	His	Ile	Met	Asp	Glu	Ala
			35					40						45		
cgc	cgt	ggc	aaa	aaa	acc	gtt	gct	gaa	ctt	atg	gaa	gaa	tgt	atg	cac	191
	Arg	Arg	Gly	Lys	Lys	Thr	Val	Ala	Glu	Leu	Met	Glu	Glu	Cys	Met	His
			50					55					60			
ttt	ttg	aaa	aaa	gat	gag	gtg	atg	ccc	ggg	gtg	ggg	aat	atg	gtc	cct	239
	Phe	Leu	Lys	Lys	Asp	Glu	Val	Met	Pro	Gly	Val	Gly	Asn	Met	Val	Pro
		65					70					75				
gat	ttg	ggc	gta	gaa	gcc	act	ttc	ccc	gat	ggc	acc	aaa	ctc	gta	acc	287
	Asp	Leu	Gly	Val	Glu	Ala	Thr	Phe	Pro	Asp	Gly	Thr	Lys	Leu	Val	Thr
	80					85				90					95	
gtg	aat	tgg	ccc	att	gaa	cct	gat	gaa	cac	ttt	aaa	gcc	ggg	gaa	gtg	335
	Val	Asn	Trp	Pro	Ile	Glu	Pro	Asp	Glu	His	Phe	Lys	Ala	Gly	Glu	Val
			100						105					110		
aaa	ttt	ggc	tgt	gat	aaa	gac	att	gag	ctc	aac	gtg	ggg	aag	gaa	gtt	383
	Lys	Phe	Gly	Cys	Asp	Lys	Asp	Ile	Glu	Leu	Asn	Val	Gly	Lys	Glu	Val
			115					120					125			
acc	gag	ctt	gaa	gtt	acc	aac	gaa	gga	cct	aaa	tcc	ttg	cat	gtg	ggg	431
	Thr	Glu	Leu	Glu	Val	Thr	Asn	Glu	Gly	Pro	Lys	Ser	Leu	His	Val	Gly
		130						135					140			
agc	cat	ttc	cac	ttc	ttt	gaa	acc	aac	aag	gca	ttg	aaa	ttc	gat	cgg	479
	Ser	His	Phe	His	Phe	Phe	Glu	Thr	Asn	Lys	Ala	Leu	Lys	Phe	Asp	Arg
		145					150				155					
gaa	aaa	gcc	tat	ggc	aaa	cgc	cta	gat	att	ccc	tct	ggc	aac	acg	cta	527
	Glu	Lys	Ala	Tyr	Gly	Lys	Arg	Leu	Asp	Ile	Pro	Ser	Gly	Asn	Thr	Leu
	160					165				170				175		
cgc	att	ggg	gca	gga	caa	acc	cgt	aaa	gtg	cag	tta	atc	cct	ctt	ggc	575

Arg Ile Gly Ala Gly Gln Thr Arg Lys Val Gln Leu Ile Pro Leu Gly	
180 185 190	
ggt agt aaa aaa gtg att ggc atg aac ggg ctt gtg aat aat att gcg	623
Gly Ser Lys Lys Val Ile Gly Met Asn Gly Leu Val Asn Asn Ile Ala	
195 200 205	
gac gaa cgc cat aaa cac aaa gca cta gac aag gca aaa tct cac gga	671
Asp Glu Arg His Lys His Lys Ala Leu Asp Lys Ala Lys Ser His Gly	
210 215 220	
ttc atc aag taa ggagactccc atg aaa atg aaa aaa caa gag tat gta	720
Phe Ile Lys Met Lys Met Lys Lys Gln Glu Tyr Val	
225 230 235	
aac acc tac gga ccc acc aca ggc gat aaa gtg cgc tta gga gat acc	768
Asn Thr Tyr Gly Pro Thr Thr Gly Asp Lys Val Arg Leu Gly Asp Thr	
240 245 250	
gat ctt tgg gca gaa gta gaa cat gac tat acc act tat ggc gaa gag	816
Asp Leu Trp Ala Glu Val Glu His Asp Tyr Thr Thr Tyr Gly Glu Glu	
255 260 265	
ctc aaa ttt ggc gcg ggt aaa act atc cgt gag ggt atg ggt cag agc	864
Leu Lys Phe Gly Ala Gly Lys Thr Ile Arg Glu Gly Met Gly Gln Ser	
270 275 280	
aat agc cca gat gaa aac acc tta gat tta gtg atc acc aac gcg atg	912
Asn Ser Pro Asp Glu Asn Thr Leu Asp Leu Val Ile Thr Asn Ala Met	
285 290 295 300	
att atc gac tac acc ggg att tat aaa gcc gac att ggt att aaa aat	960
Ile Ile Asp Tyr Thr Gly Ile Tyr Lys Ala Asp Ile Gly Ile Lys Asn	
305 310 315	
ggc aaa atc cat ggt att ggc aag gcg ggg aac aaa gac atg caa gat	1008
Gly Lys Ile His Gly Ile Gly Lys Ala Gly Asn Lys Asp Met Gln Asp	
320 325 330	
ggc gta agc cct cat atg gtc gtg ggt gtg ggc aca gaa gca cta gca	1056
Gly Val Ser Pro His Met Val Val Gly Val Gly Thr Glu Ala Leu Ala	
335 340 345	
ggg gaa ggt atg att att acc gct ggg ggg atc gat tcg cac acc cac	1104
Gly Glu Gly Met Ile Ile Thr Ala Gly Gly Ile Asp Ser His Thr His	
350 355 360	
ttc ctc tct ccc caa caa ttc cct acc gct cta gcc aat ggt gtt aca	1152

Phe Leu Ser Pro Gln Gln Phe Pro Thr Ala Leu Ala Asn Gly Val Thr	
365	370 375 380
acc atg ttt gga ggt ggc aca ggt ccg gta gat ggc acg aat gcg acc	1200
Thr Met Phe Gly Gly Gly Thr Gly Pro Val Asp Gly Thr Asn Ala Thr	
385 390 395	
acc atc act ccg ggc aaa tgg aac ttg cac cgc atg ttg cgc gca gct	1248
Thr Ile Thr Pro Gly Lys Trp Asn Leu His Arg Met Leu Arg Ala Ala	
400 405 410	
gaa gag tat tct atg aat gta ggc ttt ttg ggc aaa ggc aat agt tct	1296
Glu Glu Tyr Ser Met Asn Val Gly Phe Leu Gly Lys Gly Asn Ser Ser	
415 420 425	
agc aaa aaa caa ctt gta gaa caa gta gaa gcg ggc gcg att ggc ttt	1344
Ser Lys Lys Gln Leu Val Glu Gln Val Glu Ala Gly Ala Ile Gly Phe	
430 435 440	
aaa ttg cat gaa gac tgg ggc aca aca cca agt gcg atc gat cac tgc	1392
Lys Leu His Glu Asp Trp Gly Thr Thr Pro Ser Ala Ile Asp His Cys	
445 450 455 460	
ttg agc gtg gca gat gaa tac gat gtg caa gtt tgt atc cac acc gat	1440
Leu Ser Val Ala Asp Glu Tyr Asp Val Gln Val Cys Ile His Thr Asp	
465 470 475	
acg gtc aat gag gca ggt tat gtg gat gac acc cta aat gca atg aac	1488
Thr Val Asn Glu Ala Gly Tyr Val Asp Asp Thr Leu Asn Ala Met Asn	
480 485 490	
ggg cgc gcc atc cat gcc tac cac att gag gga gcg ggc gga gga cac	1536
Gly Arg Ala Ile His Ala Tyr His Ile Glu Gly Ala Gly Gly Gly His	
495 500 505	
tca cct gat gtt atc acc atg gca ggc gag ctc aat att cta ccc tcc	1584
Ser Pro Asp Val Ile Thr Met Ala Gly Glu Leu Asn Ile Leu Pro Ser	
510 515 520	
tcc acc acc ccc act att ccc tat acc att aat acg gtt gca gaa cac	1632
Ser Thr Thr Pro Thr Ile Pro Tyr Thr Ile Asn Thr Val Ala Glu His	
525 530 535 540	
tta gac atg ctc atg acc tgc cac cac cta gat aag cgc atc cgc gag	1680
Leu Asp Met Leu Met Thr Cys His His Leu Asp Lys Arg Ile Arg Glu	
545 550 555	
gat tta caa ttt tct caa agc cgt atc cgc ccc gga tct att gcc gct	1728

Asp Leu Gln Phe Ser Gln Ser Arg Ile Arg Pro Gly Ser Ile Ala Ala	
560	570
gag gat gtg ctc cat gat att ggc gtg atc gcg atg act agc tcc gat	1776
Glu Asp Val Leu His Asp Ile Gly Val Ile Ala Met Thr Ser Ser Asp	
575	585
tcg caa gca atg ggg cgc gct ggg gaa gtg att cct aga act tgg caa	1824
Ser Gln Ala Met Gly Arg Ala Gly Glu Val Ile Pro Arg Thr Trp Gln	
590	600
act gca gat aag aat aaa aaa gaa ttt ggt aag ctt cct gaa gat ggt	1872
Thr Ala Asp Lys Asn Lys Lys Glu Phe Gly Lys Leu Pro Glu Asp Gly	
605	615
gca gat aac gac aac ttc cgc atc aaa cgc tat atc tcc aaa tac acc	1920
Ala Asp Asn Asp Asn Phe Arg Ile Lys Arg Tyr Ile Ser Lys Tyr Thr	
625	635
att aat ccc gct ttg acc cat ggc gtg agc gag tat atc ggc tct gtg	1968
Ile Asn Pro Ala Leu Thr His Gly Val Ser Glu Tyr Ile Gly Ser Val	
640	650
gaa gag ggc aag atc gcc gac ttg gtg gtg tgg aat cct gcc ttt ttt	2016
Glu Glu Gly Lys Ile Ala Asp Leu Val Val Trp Asn Pro Ala Phe Phe	
655	665
ggc gtg aaa cct aag att gtg att aaa ggt ggc atg gtg gtc ttc tct	2064
Gly Val Lys Pro Lys Ile Val Ile Lys Gly Gly Met Val Val Phe Ser	
670	680
gaa atg ggc gat tct aac gcg tcc gtg ccc acg cct cag ccg gtt tat	2112
Glu Met Gly Asp Ser Asn Ala Ser Val Pro Thr Pro Gln Pro Val Tyr	
685	700
tac cgc gaa atg ttt ggg cac cac ggc aag gcg aaa ttt gac acc agc	2160
Tyr Arg Glu Met Phe Gly His His Gly Lys Ala Lys Phe Asp Thr Ser	
705	715
atc act ttt cgt gtc tca agc gg	2183
Ile Thr Phe Arg Val Ser Ser	
720	

<210> 8

<211> 226

<212> PRT

<213> Helicobacter felis

<400> 8

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Gly Glu Val Ala Arg Lys Arg Lys Ala Glu Gly Leu Lys Leu Asn Gln
20 25 30
Pro Glu Ala Ile Ala Tyr Ile Ser Ala His Ile Met Asp Glu Ala Arg
35 40 45
Arg Gly Lys Lys Thr Val Ala Glu Leu Met Glu Glu Cys Met His Phe
50 55 60
Leu Lys Lys Asp Glu Val Met Pro Gly Val Gly Asn Met Val Pro Asp
65 70 75 80
Leu Gly Val Glu Ala Thr Phe Pro Asp Gly Thr Lys Leu Val Thr Val
85 90 95
Asn Trp Pro Ile Glu Pro Asp Glu His Phe Lys Ala Gly Glu Val Lys
100 105 110
Phe Gly Cys Asp Lys Asp Ile Glu Leu Asn Val Gly Lys Glu Val Thr
115 120 125
Glu Leu Glu Val Thr Asn Glu Gly Pro Lys Ser Leu His Val Gly Ser
130 135 140
His Phe His Phe Phe Glu Thr Asn Lys Ala Leu Lys Phe Asp Arg Glu
145 150 155 160
Lys Ala Tyr Gly Lys Arg Leu Asp Ile Pro Ser Gly Asn Thr Leu Arg
165 170 175
Ile Gly Ala Gly Gln Thr Arg Lys Val Gln Leu Ile Pro Leu Gly Gly
180 185 190
Ser Lys Lys Val Ile Gly Met Asn Gly Leu Val Asn Asn Ile Ala Asp
195 200 205
Glu Arg His Lys His Lys Ala Leu Asp Lys Ala Lys Ser His Gly Phe
210 215 220
Ile Lys
225

<210> 9

<211> 496

<212> PRT

<213> *Helicobacter felis*

<400> 9

Met Lys Met Lys Lys Gln Glu Tyr Val Asn Thr Tyr Gly Pro Thr Thr
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20 25 30
His Asp Tyr Thr Thr Tyr Gly Glu Glu Leu Lys Phe Gly Ala Gly Lys
35 40 45
Thr Ile Arg Glu Gly Met Gly Gln Ser Asn Ser Pro Asp Glu Asn Thr
50 55 60

Leu Asp Leu Val Ile Thr Asn Ala Met Ile Ile Asp Tyr Thr Gly Ile
 65 70 75 80
 Tyr Lys Ala Asp Ile Gly Ile Lys Asn Gly Lys Ile His Gly Ile Gly
 85 90 95
 Lys Ala Gly Asn Lys Asp Met Gln Asp Gly Val Ser Pro His Met Val
 100 105 110
 Val Gly Val Gly Thr Glu Ala Leu Ala Gly Glu Gly Met Ile Ile Thr
 115 120 125
 Ala Gly Gly Ile Asp Ser His Thr His Phe Leu Ser Pro Gln Gln Phe
 130 135 140
 Pro Thr Ala Leu Ala Asn Gly Val Thr Thr Met Phe Gly Gly Gly Thr
 145 150 155 160
 Gly Pro Val Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro Gly Lys Trp
 165 170 175
 Asn Leu His Arg Met Leu Arg Ala Ala Glu Glu Tyr Ser Met Asn Val
 180 185 190
 Gly Phe Leu Gly Lys Gly Asn Ser Ser Ser Lys Lys Gln Leu Val Glu
 195 200 205
 Gln Val Glu Ala Gly Ala Ile Gly Phe Lys Leu His Glu Asp Trp Gly
 210 215 220
 Thr Thr Pro Ser Ala Ile Asp His Cys Leu Ser Val Ala Asp Glu Tyr
 225 230 235 240
 Asp Val Gln Val Cys Ile His Thr Asp Thr Val Asn Glu Ala Gly Tyr
 245 250 255
 Val Asp Asp Thr Leu Asn Ala Met Asn Gly Arg Ala Ile His Ala Tyr
 260 265 270
 His Ile Glu Gly Ala Gly Gly Gly His Ser Pro Asp Val Ile Thr Met
 275 280 285
 Ala Gly Glu Leu Asn Ile Leu Pro Ser Ser Thr Thr Pro Thr Ile Pro
 290 295 300
 Tyr Thr Ile Asn Thr Val Ala Glu His Leu Asp Met Leu Met Thr Cys
 305 310 315 320
 His His Leu Asp Lys Arg Ile Arg Glu Asp Leu Gln Phe Ser Gln Ser
 325 330 335
 Arg Ile Arg Pro Gly Ser Ile Ala Ala Glu Asp Val Leu His Asp Ile
 340 345 350
 Gly Val Ile Ala Met Thr Ser Ser Asp Ser Gln Ala Met Gly Arg Ala
 355 360 365
 Gly Glu Val Ile Pro Arg Thr Trp Gln Thr Ala Asp Lys Asn Lys Lys
 370 375 380
 Glu Phe Gly Lys Leu Pro Glu Asp Gly Ala Asp Asn Asp Asn Phe Arg
 385 390 395 400
 Ile Lys Arg Tyr Ile Ser Lys Tyr Thr Ile Asn Pro Ala Leu Thr His
 405 410 415
 Gly Val Ser Glu Tyr Ile Gly Ser Val Glu Glu Gly Lys Ile Ala Asp
 420 425 430
 Leu Val Val Trp Asn Pro Ala Phe Phe Gly Val Lys Pro Lys Ile Val
 435 440 445

Ile Lys Gly Gly Met Val Val Phe Ser Glu Met Gly Asp Ser Asn Ala
 450 455 460
 Ser Val Pro Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met Phe Gly His
 465 470 475 480
 His Gly Lys Ala Lys Phe Asp Thr Ser Ile Thr Phe Arg Val Ser Ser
 485 490 495

<210> 10
 <211> 2407
 <212> DNA
 <213> Helicobacter felis

<220>
 <221> CDS
 <222> (2)..(682)

<220>
 <221> CDS
 <222> (693)..(2399)

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 Val Lys Leu Thr Pro Lys Glu Gln Glu Lys Phe Leu Leu Tyr Tyr Ala
 1 5 10 15
 ggc gaa gtg gct aga aag cgc aaa gcg gag ggc tta aag ctc aac caa 97
 Gly Glu Val Ala Arg Lys Arg Lys Ala Glu Gly Leu Lys Leu Asn Gln
 20 25 30
 ccc gaa gcc att gcc tac att agt gcc cat att atg gac gag gcg cgc 145
 Pro Glu Ala Ile Ala Tyr Ile Ser Ala His Ile Met Asp Glu Ala Arg
 35 40 45
 cgt ggc aaa aag acc gtt gcg gaa ctt atg gaa gag tgt atg cac ttt 193
 Arg Gly Lys Lys Thr Val Ala Glu Leu Met Glu Glu Cys Met His Phe
 50 55 60
 ttg aaa aaa gac gag gtg atg ccc ggt gtg ggg aat atg gtc cct gat 241
 Leu Lys Lys Asp Glu Val Met Pro Gly Val Gly Asn Met Val Pro Asp
 65 70 75 80
 tta ggc gtg gaa gct act ttt ccc gat ggc acc aaa ctc gta acc gtg 289
 Leu Gly Val Glu Ala Thr Phe Pro Asp Gly Thr Lys Leu Val Thr Val
 85 90 95
 aat tgg ccc atc gaa ccc gat gaa cac ttc aaa gcg ggc gaa gtc aaa 337

Asn Trp Pro Ile Glu Pro Asp Glu His Phe Lys Ala Gly Glu Val Lys	
100	105 110
ttt ggc tgt gat aaa gac att gaa ctc aac gca ggt aag gaa gtt acc	385
Phe Gly Cys Asp Lys Asp Ile Glu Leu Asn Ala Gly Lys Glu Val Thr	
115	120 125
gaa cta gaa gtt acc aac gaa gga cct aaa tcc ttg cat gtg ggt agc	433
Glu Leu Glu Val Thr Asn Glu Gly Pro Lys Ser Leu His Val Gly Ser	
130	135 140
cat ttc cac ttc ttt gaa gcc aac aag gca ttg aaa ttc gat cgg gaa	481
His Phe His Phe Phe Glu Ala Asn Lys Ala Leu Lys Phe Asp Arg Glu	
145	150 155 160
aaa gcc tat ggc aaa cgc cta gat att ccc tct ggc aac acg cta cgc	529
Lys Ala Tyr Gly Lys Arg Leu Asp Ile Pro Ser Gly Asn Thr Leu Arg	
165	170 175
att ggg gca gga caa acc cgt aaa gtg cag tta atc cct ctt ggc ggc	577
Ile Gly Ala Gly Gln Thr Arg Lys Val Gln Leu Ile Pro Leu Gly Gly	
180	185 190
agt aaa aaa gtg att ggc atg aac ggg ctt gtg aat aat att gca gat	625
Ser Lys Lys Val Ile Gly Met Asn Gly Leu Val Asn Asn Ile Ala Asp	
195	200 205
gaa cgc cat aaa cac aaa gcg tta gaa aaa gca aaa tct cac gga ttt	673
Glu Arg His Lys His Lys Ala Leu Glu Lys Ala Lys Ser His Gly Phe	
210	215 220
atc aaa taa ggagactccc atg aaa atg aaa aaa caa gag tat gta aat	722
Ile Lys Met Lys Met Lys Lys Gln Glu Tyr Val Asn	
225	230 235
acc tac gga cct acc aca ggc gac aaa gtg cgc tta gga gat acc gat	770
Thr Tyr Gly Pro Thr Thr Gly Asp Lys Val Arg Leu Gly Asp Thr Asp	
240	245 250
ctt tgg gca gaa gta gaa cat gac tat acc act tat ggc gaa gag ctc	818
Leu Trp Ala Glu Val Glu His Asp Tyr Thr Thr Tyr Gly Glu Glu Leu	
255	260 265
aaa ttt ggc gcg ggt aaa act atc cgt gag ggc atg ggt cag agc aat	866
Lys Phe Gly Ala Gly Lys Thr Ile Arg Glu Gly Met Gly Gln Ser Asn	
270	275 280 285
agt cca gat gaa aac acc cta gat tta gtc atc acc aac gcg atg att	914

Ser Pro Asp Glu Asn Thr Leu Asp Leu Val Ile Thr Asn Ala Met Ile	
290 295 300	
att gac tac acc ggg att tac aaa gcc gac att ggc att aaa aat ggc	962
Ile Asp Tyr Thr Gly Ile Tyr Lys Ala Asp Ile Gly Ile Lys Asn Gly	
305 310 315	
aaa atc cat ggc att ggc aag gca gga aac aag gac atg caa gat ggc	1010
Lys Ile His Gly Ile Gly Lys Ala Gly Asn Lys Asp Met Gln Asp Gly	
320 325 330	
gta agc cct cat atg gtc gtg ggt gtg ggc aca gaa gca tta gca ggg	1058
Val Ser Pro His Met Val Val Gly Val Gly Thr Glu Ala Leu Ala Gly	
335 340 345	
gaa ggt atg att att acc gct ggg ggg atc gat tca cac acc cac ttc	1106
Glu Gly Met Ile Ile Thr Ala Gly Gly Ile Asp Ser His Thr His Phe	
350 355 360 365	
ctc tct cca caa caa ttc cct acc gct cta gcc aat ggc gtt aca acc	1154
Leu Ser Pro Gln Gln Phe Pro Thr Ala Leu Ala Asn Gly Val Thr Thr	
370 375 380	
atg ttt ggc ggt ggc aca ggt ccg gta gat ggc acg aat gcg act acc	1202
Met Phe Gly Gly Gly Thr Gly Pro Val Asp Gly Thr Asn Ala Thr Thr	
385 390 395	
atc act ccg ggc aaa tgg aac ttg cac cgc atg ttg cgc gca gct gaa	1250
Ile Thr Pro Gly Lys Trp Asn Leu His Arg Met Leu Arg Ala Ala Glu	
400 405 410	
gag tat tct atg aat gtg ggc ttt ttg ggc aaa ggc aat agc tcc agt	1298
Glu Tyr Ser Met Asn Val Gly Phe Leu Gly Lys Gly Asn Ser Ser Ser	
415 420 425	
aaa aaa caa ctt gta gaa caa ata gaa gcg ggc gcg atc ggc ttt aaa	1346
Lys Lys Gln Leu Val Glu Gln Ile Glu Ala Gly Ala Ile Gly Phe Lys	
430 435 440 445	
ttg cat gaa gac tgg ggc aca act cca agt gca atc gat cac tgc ttg	1394
Leu His Glu Asp Trp Gly Thr Thr Pro Ser Ala Ile Asp His Cys Leu	
450 455 460	
agc gta gca gat gaa tac gat gtg caa gtt tgt atc cac acc gat acg	1442
Ser Val Ala Asp Glu Tyr Asp Val Gln Val Cys Ile His Thr Asp Thr	
465 470 475	
gtc aat gag gca ggt tat gta gat gac acc ctg aat gcg atg aac ggg	1490

Val Asn Glu Ala Gly Tyr Val Asp Asp Thr Leu Asn Ala Met Asn Gly	
480 485 490	
cgc gcc atc cat gcc tac cac att gag gga gcg ggc gga gga cac tca	1538
Arg Ala Ile His Ala Tyr His Ile Glu Gly Ala Gly Gly Gly His Ser	
495 500 505	
cct gat gtt atc acc atg gca ggc gag ctc aat att cta ccc tcc tcc	1586
Pro Asp Val Ile Thr Met Ala Gly Glu Leu Asn Ile Leu Pro Ser Ser	
510 515 520 525	
aca acc ccc act atc ccc tat acc att aat acg gtt gca gaa cac tta	1634
Thr Thr Pro Thr Ile Pro Tyr Thr Ile Asn Thr Val Ala Glu His Leu	
530 535 540	
gac atg ctc atg acc tgc cac cac cta gat aaa cgc atc cgc gag gat	1682
Asp Met Leu Met Thr Cys His His Leu Asp Lys Arg Ile Arg Glu Asp	
545 550 555	
tta caa ttt tcc caa agc cgt atc cgc ccc ggc tct atc gcc gct gaa	1730
Leu Gln Phe Ser Gln Ser Arg Ile Arg Pro Gly Ser Ile Ala Ala Glu	
560 565 570	
gat gtg ctc cat gat att ggc gtg atc gcg atg aca agc tcg gat tcg	1778
Asp Val Leu His Asp Ile Gly Val Ile Ala Met Thr Ser Ser Asp Ser	
575 580 585	
caa gca atg ggg cgc gct ggc gaa gtg att cct cga act tgg cag act	1826
Gln Ala Met Gly Arg Ala Gly Glu Val Ile Pro Arg Thr Trp Gln Thr	
590 595 600 605	
gcg gat aag aat aaa aaa gaa ttt ggt aag ctt cct gaa gat agt gca	1874
Ala Asp Lys Asn Lys Lys Glu Phe Gly Lys Leu Pro Glu Asp Ser Ala	
610 615 620	
gat aac gac aac ttc cgt atc aaa cgc tac atc tcc aaa tac act att	1922
Asp Asn Asp Asn Phe Arg Ile Lys Arg Tyr Ile Ser Lys Tyr Thr Ile	
625 630 635	
aac ccc gct cta acc cat ggg gta agc gag tat atc ggc tct gtg gaa	1970
Asn Pro Ala Leu Thr His Gly Val Ser Glu Tyr Ile Gly Ser Val Glu	
640 645 650	
gag ggc aaa atc gct gat ttg gtg gtg tgg aat cct gcc ttt ttt ggt	2018
Glu Gly Lys Ile Ala Asp Leu Val Val Trp Asn Pro Ala Phe Phe Gly	
655 660 665	
gtg aaa cct aag att gtg atc aaa ggc ggt atg gtg gtc ttc tct gaa	2066

Val	Lys	Pro	Lys	Ile	Val	Ile	Lys	Gly	Gly	Met	Val	Val	Phe	Ser	Glu
670					675					680					685
atg ggc gac tcc aac gcg tcc gtg cct aca cct cag ccg gtt tat tac	2114														
Met Gly Asp Ser Asn Ala Ser Val Pro Thr Pro Gln Pro Val Tyr Tyr															
690 695 700															
cgc gaa atg ttt ggg cat cac gcc aag gcg aaa ttt gac acc agc atc	2162														
Arg Glu Met Phe Gly His His Gly Lys Ala Lys Phe Asp Thr Ser Ile															
705 710 715															
act ttt gtt tcc aaa gtc gcc tat gaaaat gccgtgaaa gaa aaa cta	2210														
Thr Phe Val Ser Lys Val Ala Tyr GluAsnGlyValLysGluLysLeu															
720 725 730															
ggc tta gag cgc aag gtg ctacccgtgaaa aactgc cgc aac atc act	2258														
Gly Leu Glu Arg Lys Val Leu Pro Val Lys AsnCysArgAsnIleThr															
735 740 745															
aag aaa gac ttc aaa ttc aac aac aag acg gcgcatatc act gtc gat	2306														
Lys Lys Asp Phe Lys Phe Asn Asn Lys ThrAlaHisIleThrValAsp															
750 755 760 765															
cct aaa acc ttc gag gtc ttt gta gatgccaaa ctctgcacc tct aaa	2354														
Pro Lys ThrPheGluValPheValAspGlyLysLeuCysThrSerLys															
770 775 780															
ccc gcc tct gaa gtg cct cta gcc cag cgctaccttcttc ttctag	2399														
Pro Ala SerGluValProLeuAlaGlnArgTyrThrPhePhe															
785 790 795															
gcncgaatg	2407														

Leu Lys Lys Asp Glu Val Met Pro Gly Val Gly Asn Met Val Pro Asp
 65 70 75 80
 Leu Gly Val Glu Ala Thr Phe Pro Asp Gly Thr Lys Leu Val Thr Val
 85 90 95
 Asn Trp Pro Ile Glu Pro Asp Glu His Phe Lys Ala Gly Glu Val Lys
 100 105 110
 Phe Gly Cys Asp Lys Asp Ile Glu Leu Asn Ala Gly Lys Glu Val Thr
 115 120 125
 Glu Leu Glu Val Thr Asn Glu Gly Pro Lys Ser Leu His Val Gly Ser
 130 135 140
 His Phe His Phe Phe Glu Ala Asn Lys Ala Leu Lys Phe Asp Arg Glu
 145 150 155 160
 Lys Ala Tyr Gly Lys Arg Leu Asp Ile Pro Ser Gly Asn Thr Leu Arg
 165 170 175
 Ile Gly Ala Gly Gln Thr Arg Lys Val Gln Leu Ile Pro Leu Gly Gly
 180 185 190
 Ser Lys Lys Val Ile Gly Met Asn Gly Leu Val Asn Asn Ile Ala Asp
 195 200 205
 Glu Arg His Lys His Lys Ala Leu Glu Lys Ala Lys Ser His Gly Phe
 210 215 220
 Ile Lys
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<210> 12

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<212> PRT

<213> *Helicobacter felis*

<400> 12

Met Lys Met Lys Lys Gln Glu Tyr Val Asn Thr Tyr Gly Pro Thr Thr
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 20 25 30
 His Asp Tyr Thr Thr Tyr Gly Glu Glu Leu Lys Phe Gly Ala Gly Lys
 35 40 45
 Thr Ile Arg Glu Gly Met Gly Gln Ser Asn Ser Pro Asp Glu Asn Thr
 50 55 60
 Leu Asp Leu Val Ile Thr Asn Ala Met Ile Ile Asp Tyr Thr Gly Ile
 65 70 75 80
 Tyr Lys Ala Asp Ile Gly Ile Lys Asn Gly Lys Ile His Gly Ile Gly
 85 90 95
 Lys Ala Gly Asn Lys Asp Met Gln Asp Gly Val Ser Pro His Met Val
 100 105 110
 Val Gly Val Gly Thr Glu Ala Leu Ala Gly Glu Gly Met Ile Ile Thr
 115 120 125
 Ala Gly Gly Ile Asp Ser His Thr His Phe Leu Ser Pro Gln Gln Phe
 130 135 140

Pro Thr Ala Leu Ala Asn Gly Val Thr Thr Met Phe Gly Gly Gly Thr																			
145					150				155									160	
Gly Pro Val Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro Gly Lys Trp																			
				165					170									175	
Asn Leu His Arg Met Leu Arg Ala Ala Glu Glu Tyr Ser Met Asn Val																			
			180					185									190		
Gly Phe Leu Gly Lys Gly Asn Ser Ser Ser Lys Lys Gln Leu Val Glu																			
		195					200								205				
Gln Ile Glu Ala Gly Ala Ile Gly Phe Lys Leu His Glu Asp Trp Gly																			
		210					215								220				
Thr Thr Pro Ser Ala Ile Asp His Cys Leu Ser Val Ala Asp Glu Tyr																			
225					230							235						240	
Asp Val Gln Val Cys Ile His Thr Asp Thr Val Asn Glu Ala Gly Tyr																			
				245					250									255	
Val Asp Asp Thr Leu Asn Ala Met Asn Gly Arg Ala Ile His Ala Tyr																			
			260					265									270		
His Ile Glu Gly Ala Gly Gly Gly His Ser Pro Asp Val Ile Thr Met																			
		275					280										285		
Ala Gly Glu Leu Asn Ile Leu Pro Ser Ser Thr Thr Pro Thr Ile Pro																			
		290					295								300				
Tyr Thr Ile Asn Thr Val Ala Glu His Leu Asp Met Leu Met Thr Cys																			
305					310							315						320	
His His Leu Asp Lys Arg Ile Arg Glu Asp Leu Gln Phe Ser Gln Ser																			
				325					330									335	
Arg Ile Arg Pro Gly Ser Ile Ala Ala Glu Asp Val Leu His Asp Ile																			
			340					345									350		
Gly Val Ile Ala Met Thr Ser Ser Asp Ser Gln Ala Met Gly Arg Ala																			
		355					360										365		
Gly Glu Val Ile Pro Arg Thr Trp Gln Thr Ala Asp Lys Asn Lys Lys																			
		370					375								380				
Glu Phe Gly Lys Leu Pro Glu Asp Ser Ala Asp Asn Asp Asn Phe Arg																			
385					390							395						400	
Ile Lys Arg Tyr Ile Ser Lys Tyr Thr Ile Asn Pro Ala Leu Thr His																			
				405					410									415	
Gly Val Ser Glu Tyr Ile Gly Ser Val Glu Glu Gly Lys Ile Ala Asp																			
			420					425										430	
Leu Val Val Trp Asn Pro Ala Phe Phe Gly Val Lys Pro Lys Ile Val																			
		435					440										445		
Ile Lys Gly Gly Met Val Val Phe Ser Glu Met Gly Asp Ser Asn Ala																			
		450				455						460							
Ser Val Pro Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met Phe Gly His																			
465					470						475							480	
His Gly Lys Ala Lys Phe Asp Thr Ser Ile Thr Phe Val Ser Lys Val																			
				485					490									495	
Ala Tyr Glu Asn Gly Val Lys Glu Lys Leu Gly Leu Glu Arg Lys Val																			
			500					505									510		
Leu Pro Val Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp Phe Lys Phe																			
			515					520										525	

Asn	Asn	Lys	Thr	Ala	His	Ile	Thr	Val	Asp	Pro	Lys	Thr	Phe	Glu	Val
530						535					540				
Phe	Val	Asp	Gly	Lys	Leu	Cys	Thr	Ser	Lys	Pro	Ala	Ser	Glu	Val	Pro
545					550					555					560
Leu	Ala	Gln	Arg	Tyr	Thr	Phe	Phe								
				565											

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 <213> Helicobacter felis

<220>
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<220>
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 <222> (739)..(2445)

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 Val Lys Leu
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aca ccc aaa gag caa gaa aag ttc ttg tta tat tat gcg ggc gaa gtg 104
 Thr Pro Lys Glu Gln Glu Lys Phe Leu Leu Tyr Tyr Ala Gly Glu Val
 5 10 15

gct aga aag cgc aaa gca gag ggc tta aag ctc aac caa ccc gaa gcc 152
 Ala Arg Lys Arg Lys Ala Glu Gly Leu Lys Leu Asn Gln Pro Glu Ala
 20 25 30 35

att gcc tac att agt gcc cat att atg gac gag gcg cgt cgt ggc aaa 200
 Ile Ala Tyr Ile Ser Ala His Ile Met Asp Glu Ala Arg Arg Gly Lys
 40 45 50

aaa acc gtt gcg gaa ctt atg gaa gag tgt atg cac ttt ttg aaa aaa 248
 Lys Thr Val Ala Glu Leu Met Glu Glu Cys Met His Phe Leu Lys Lys
 55 60 65

gac gag gtg atg ccc ggg gtg ggg aat atg gtc cct gat ttg ggc gtg 296
 Asp Glu Val Met Pro Gly Val Gly Asn Met Val Pro Asp Leu Gly Val
 70 75 80

gaa gcc act ttc ccc gat ggc acc aaa ctc gta act gtg aat tgg ccc 344

Glu	Ala	Thr	Phe	Pro	Asp	Gly	Thr	Lys	Leu	Val	Thr	Val	Asn	Trp	Pro	
85						90						95				
atc	gaa	cct	gat	gaa	cac	ttt	aag	gcg	ggt	gaa	gtg	aaa	ttt	ggc	tgt	392
Ile	Glu	Pro	Asp	Glu	His	Phe	Lys	Ala	Gly	Glu	Val	Lys	Phe	Gly	Cys	
100					105					110					115	
gat	aaa	gac	att	gaa	ctc	aac	gca	ggt	aag	gaa	ggt	acc	gaa	cta	gaa	440
Asp	Lys	Asp	Ile	Glu	Leu	Asn	Ala	Gly	Lys	Glu	Val	Thr	Glu	Leu	Glu	
				120					125					130		
gtt	act	aac	gaa	gga	cct	aaa	tcc	ttg	cat	gtg	ggt	agc	cat	ttc	cac	488
Val	Thr	Asn	Glu	Gly	Pro	Lys	Ser	Leu	His	Val	Gly	Ser	His	Phe	His	
			135					140					145			
ttc	ttt	gaa	gcc	aac	aaa	gca	ttg	aaa	ttc	gat	cgg	gaa	aaa	gcc	tat	536
Phe	Phe	Glu	Ala	Asn	Lys	Ala	Leu	Lys	Phe	Asp	Arg	Glu	Lys	Ala	Tyr	
		150					155					160				
ggc	aaa	cgc	cta	gat	att	ccc	tct	ggc	aac	aca	cta	cgc	att	ggg	gca	584
Gly	Lys	Arg	Leu	Asp	Ile	Pro	Ser	Gly	Asn	Thr	Leu	Arg	Ile	Gly	Ala	
	165					170					175					
gga	caa	acc	cgt	aaa	gtg	cag	tta	atc	cct	ctt	ggc	ggt	agt	aaa	aaa	632
Gly	Gln	Thr	Arg	Lys	Val	Gln	Leu	Ile	Pro	Leu	Gly	Gly	Ser	Lys	Lys	
180					185					190					195	
gtg	att	ggc	atg	aac	ggg	ctt	gtg	aat	aat	att	gcg	gac	gaa	cgc	cat	680
Val	Ile	Gly	Met	Asn	Gly	Leu	Val	Asn	Asn	Ile	Ala	Asp	Glu	Arg	His	
				200					205					210		
aaa	cac	aaa	gcg	cta	gac	aaa	gca	aaa	tct	cac	gga	ttt	atc	aag	taa	728
Lys	His	Lys	Ala	Leu	Asp	Lys	Ala	Lys	Ser	His	Gly	Phe	Ile	Lys		
		215						220				225				
ggagactccc	atg	aaa	atg	aaa	aaa	caa	gag	tat	gta	aat	acc	tac	gga			777
	Met	Lys	Met	Lys	Lys	Gln	Glu	Tyr	Val	Asn	Thr	Tyr	Gly			
				230					235				240			
ccc	acc	aca	ggc	gat	aaa	gtg	cgc	tta	gga	gat	acc	gat	ctt	tgg	gca	825
Pro	Thr	Thr	Gly	Asp	Lys	Val	Arg	Leu	Gly	Asp	Thr	Asp	Leu	Trp	Ala	
			245						250					255		
gaa	gta	gaa	cat	gac	tat	acc	acc	tat	ggc	gaa	gaa	ctc	aaa	ttc	ggt	873
Glu	Val	Glu	His	Asp	Tyr	Thr	Thr	Tyr	Gly	Glu	Glu	Leu	Lys	Phe	Gly	
			260					265					270			
gca	ggt	aaa	act	atc	cgt	gag	ggt	atg	ggt	cag	agc	aat	agc	cca	gat	921

Ala Gly Lys Thr Ile Arg Glu Gly Met Gly Gln Ser Asn Ser Pro Asp	
275	280 285
gaa aac acc tta gat tta gtg atc acc aac gcg atg att att gac tac	969
Glu Asn Thr Leu Asp Leu Val Ile Thr Asn Ala Met Ile Ile Asp Tyr	
290	295 300
acc ggg att tac aaa gcc gac att ggc att aaa aat ggc aaa atc cat	1017
Thr Gly Ile Tyr Lys Ala Asp Ile Gly Ile Lys Asn Gly Lys Ile His	
305	310 315 320
ggc att ggc aag gca gga aac aag gac atg caa gat ggc gta agc cct	1065
Gly Ile Gly Lys Ala Gly Asn Lys Asp Met Gln Asp Gly Val Ser Pro	
	325 330 335
cat atg gtc gtg ggt gtg ggc aca gaa gca cta gca ggg gaa ggt atg	1113
His Met Val Val Gly Val Gly Thr Glu Ala Leu Ala Gly Glu Gly Met	
	340 345 350
att att acc gct ggg ggg atc gat tca cac acc cac ttc ctc tct cca	1161
Ile Ile Thr Ala Gly Gly Ile Asp Ser His Thr His Phe Leu Ser Pro	
	355 360 365
caa caa ttc cct acc gct cta gcc aat ggc gtt aca aca atg ttt ggc	1209
Gln Gln Phe Pro Thr Ala Leu Ala Asn Gly Val Thr Thr Met Phe Gly	
	370 375 380
ggt ggc aca ggc ccc gta gat ggc acg aat gcg act acc atc act ccg	1257
Gly Gly Thr Gly Pro Val Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro	
385	390 395 400
ggc aaa tgg aac ttg cac cgc atg ttg cgc gca gca gaa gag tat tct	1305
Gly Lys Trp Asn Leu His Arg Met Leu Arg Ala Ala Glu Glu Tyr Ser	
	405 410 415
atg aat gtg ggc ttt ttg ggc aaa ggc aat agc tct agt aaa aaa caa	1353
Met Asn Val Gly Phe Leu Gly Lys Gly Asn Ser Ser Ser Lys Lys Gln	
	420 425 430
ctt gta gaa caa gta gaa gcg ggc gcg att ggt ttt aaa ttg cat gaa	1401
Leu Val Glu Gln Val Glu Ala Gly Ala Ile Gly Phe Lys Leu His Glu	
	435 440 445
gac tgg ggc aca act cca agt gcg atc gat cac tgc ttg agc gta gca	1449
Asp Trp Gly Thr Thr Pro Ser Ala Ile Asp His Cys Leu Ser Val Ala	
450	455 460
gat gaa tac gat gtg caa gtt tgt ata cac acc gat acg gtc aat gag	1497

Asp	Glu	Tyr	Asp	Val	Gln	Val	Cys	Ile	His	Thr	Asp	Thr	Val	Asn	Glu	
465					470					475					480	
gca	ggt	tat	gta	gat	gac	acc	cta	aat	gca	atg	aac	ggg	cgc	gcc	atc	1545
Ala	Gly	Tyr	Val	Asp	Asp	Thr	Leu	Asn	Ala	Met	Asn	Gly	Arg	Ala	Ile	
				485					490					495		
cat	gcc	tac	cac	att	gag	gga	gcg	ggt	gga	gga	cac	tca	cct	gat	gtt	1593
His	Ala	Tyr	His	Ile	Glu	Gly	Ala	Gly	Gly	Gly	His	Ser	Pro	Asp	Val	
			500					505					510			
atc	acc	atg	gca	ggc	gaa	gtg	aat	att	cta	ccc	tcc	tcc	aca	acc	cct	1641
Ile	Thr	Met	Ala	Gly	Glu	Val	Asn	Ile	Leu	Pro	Ser	Ser	Thr	Thr	Pro	
		515					520					525				
act	atc	ccc	tat	acc	att	aat	acg	gtt	gca	gaa	cac	tta	gac	atg	ctt	1689
Thr	Ile	Pro	Tyr	Thr	Ile	Asn	Thr	Val	Ala	Glu	His	Leu	Asp	Met	Leu	
	530					535					540					
atg	acc	tgc	cac	cac	cta	gat	aaa	cgc	atc	cgc	gag	gat	ctc	caa	ttt	1737
Met	Thr	Cys	His	His	Leu	Asp	Lys	Arg	Ile	Arg	Glu	Asp	Leu	Gln	Phe	
545					550					555					560	
tct	caa	agc	cgt	atc	cgc	ccc	ggc	tct	atc	gcc	gct	gaa	gat	gtg	ctc	1785
Ser	Gln	Ser	Arg	Ile	Arg	Pro	Gly	Ser	Ile	Ala	Ala	Glu	Asp	Val	Leu	
			565						570					575		
cat	gat	atc	ggt	gtg	atc	gcg	atg	aca	agt	tcc	gat	tcg	caa	gca	atg	1833
His	Asp	Ile	Gly	Val	Ile	Ala	Met	Thr	Ser	Ser	Asp	Ser	Gln	Ala	Met	
			580					585					590			
ggg	cgc	gct	ggg	gaa	gtg	att	cct	aga	act	tgg	caa	act	gca	gac	aag	1881
Gly	Arg	Ala	Gly	Glu	Val	Ile	Pro	Arg	Thr	Trp	Gln	Thr	Ala	Asp	Lys	
		595					600					605				
aat	aaa	aaa	gaa	ttt	ggt	aag	ctt	cct	gaa	gat	ggt	gca	gat	aat	gac	1929
Asn	Lys	Lys	Glu	Phe	Gly	Lys	Leu	Pro	Glu	Asp	Gly	Ala	Asp	Asn	Asp	
	610					615					620					
aac	ttc	cgc	atc	aaa	cgc	tat	atc	tcc	aaa	tac	acc	att	aat	ccc	gct	1977
Asn	Phe	Arg	Ile	Lys	Arg	Tyr	Ile	Ser	Lys	Tyr	Thr	Ile	Asn	Pro	Ala	
625					630					635					640	
ttg	acc	cat	ggc	gtg	agc	gag	tat	atc	ggc	tct	gtg	gaa	gag	ggc	aag	2025
Leu	Thr	His	Gly	Val	Ser	Glu	Tyr	Ile	Gly	Ser	Val	Glu	Glu	Gly	Lys	
			645						650					655		
atc	qcc	gac	ttg	gtg	gtg	tgg	aat	cct	gcc	ttt	ttt	ggc	gta	aaa	ccc	2073

Ile Ala Asp Leu Val Val Trp Asn Pro Ala Phe Phe Gly Val Lys Pro
 660 665 670
 aaa atc gtg atc aaa ggc ggt atg gtg gtg ttc tct gaa atg ggc gat 2121
 Lys Ile Val Ile Lys Gly Gly Met Val Val Phe Ser Glu Met Gly Asp
 675 680 685
 tct aat gcg tct gtg ccc act cct cag ccg gtt tat tac cgc gaa atg 2169
 Ser Asn Ala Ser Val Pro Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met
 690 695 700
 ttt ggg cat cac ggc aag gcg aaa ttt gac acc agc atc act ttt gtt 2217
 Phe Gly His His Gly Lys Ala Lys Phe Asp Thr Ser Ile Thr Phe Val
 705 710 715 720
 tcc aaa gtc gcc tat gaa aat ggt gtg aaa gaa aaa cta ggt tta gag 2265
 Ser Lys Val Ala Tyr Glu Asn Gly Val Lys Glu Lys Leu Gly Leu Glu
 725 730 735
 cgc aag gtg ctc ccc gtg aaa aac tgc cgt aac atc acc aag aag gac 2313
 Arg Lys Val Leu Pro Val Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp
 740 745 750
 ttc aag ttc aac gac aaa act gca aaa atc acc gtc gat ccg aaa acc 2361
 Phe Lys Phe Asn Asp Lys Thr Ala Lys Ile Thr Val Asp Pro Lys Thr
 755 760 765
 ttc gag gtc ttt gta gat ggc aaa ctc tgc acc tct aaa ccc acc tct 2409
 Phe Glu Val Phe Val Asp Gly Lys Leu Cys Thr Ser Lys Pro Thr Ser
 770 775 780
 gaa gtg cct cta gcc caa cgc tac act ttc ttc tag gcataat 2452
 Glu Val Pro Leu Ala Gln Arg Tyr Thr Phe Phe
 785 790 795

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<211> 226

<212> PRT

<213> *Helicobacter felis*

<400> 14

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 20 25 30
 Pro Glu Ala Ile Ala Tyr Ile Ser Ala His Ile Met Asp Glu Ala Arg
 35 40 45

Arg Gly Lys Lys Thr Val Ala Glu Leu Met Glu Glu Cys Met His Phe
 50 55 60
 Leu Lys Lys Asp Glu Val Met Pro Gly Val Gly Asn Met Val Pro Asp
 65 70 75 80
 Leu Gly Val Glu Ala Thr Phe Pro Asp Gly Thr Lys Leu Val Thr Val
 85 90 95
 Asn Trp Pro Ile Glu Pro Asp Glu His Phe Lys Ala Gly Glu Val Lys
 100 105 110
 Phe Gly Cys Asp Lys Asp Ile Glu Leu Asn Ala Gly Lys Glu Val Thr
 115 120 125
 Glu Leu Glu Val Thr Asn Glu Gly Pro Lys Ser Leu His Val Gly Ser
 130 135 140
 His Phe His Phe Phe Glu Ala Asn Lys Ala Leu Lys Phe Asp Arg Glu
 145 150 155 160
 Lys Ala Tyr Gly Lys Arg Leu Asp Ile Pro Ser Gly Asn Thr Leu Arg
 165 170 175
 Ile Gly Ala Gly Gln Thr Arg Lys Val Gln Leu Ile Pro Leu Gly Gly
 180 185 190
 Ser Lys Lys Val Ile Gly Met Asn Gly Leu Val Asn Asn Ile Ala Asp
 195 200 205
 Glu Arg His Lys His Lys Ala Leu Asp Lys Ala Lys Ser His Gly Phe
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 Ile Lys
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<210> 15

<211> 568

<212> PRT

<213> *Helicobacter felis*

<400> 15

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 His Asp Tyr Thr Thr Tyr Gly Glu Glu Leu Lys Phe Gly Ala Gly Lys
 35 40 45
 Thr Ile Arg Glu Gly Met Gly Gln Ser Asn Ser Pro Asp Glu Asn Thr
 50 55 60
 Leu Asp Leu Val Ile Thr Asn Ala Met Ile Ile Asp Tyr Thr Gly Ile
 65 70 75 80
 Tyr Lys Ala Asp Ile Gly Ile Lys Asn Gly Lys Ile His Gly Ile Gly
 85 90 95
 Lys Ala Gly Asn Lys Asp Met Gln Asp Gly Val Ser Pro His Met Val
 100 105 110
 Val Gly Val Gly Thr Glu Ala Leu Ala Gly Glu Gly Met Ile Ile Thr
 115 120 125

Ala Gly Gly Ile Asp Ser His Thr His Phe Leu Ser Pro Gln Gln Phe
 130 135 140
 Pro Thr Ala Leu Ala Asn Gly Val Thr Thr Met Phe Gly Gly Gly Thr
 145 150 155 160
 Gly Pro Val Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro Gly Lys Trp
 165 170 175
 Asn Leu His Arg Met Leu Arg Ala Ala Glu Glu Tyr Ser Met Asn Val
 180 185 190
 Gly Phe Leu Gly Lys Gly Asn Ser Ser Ser Lys Lys Gln Leu Val Glu
 195 200 205
 Gln Val Glu Ala Gly Ala Ile Gly Phe Lys Leu His Glu Asp Trp Gly
 210 215 220
 Thr Thr Pro Ser Ala Ile Asp His Cys Leu Ser Val Ala Asp Glu Tyr
 225 230 235 240
 Asp Val Gln Val Cys Ile His Thr Asp Thr Val Asn Glu Ala Gly Tyr
 245 250 255
 Val Asp Asp Thr Leu Asn Ala Met Asn Gly Arg Ala Ile His Ala Tyr
 260 265 270
 His Ile Glu Gly Ala Gly Gly Gly His Ser Pro Asp Val Ile Thr Met
 275 280 285
 Ala Gly Glu Val Asn Ile Leu Pro Ser Ser Thr Thr Pro Thr Ile Pro
 290 295 300
 Tyr Thr Ile Asn Thr Val Ala Glu His Leu Asp Met Leu Met Thr Cys
 305 310 315 320
 His His Leu Asp Lys Arg Ile Arg Glu Asp Leu Gln Phe Ser Gln Ser
 325 330 335
 Arg Ile Arg Pro Gly Ser Ile Ala Ala Glu Asp Val Leu His Asp Ile
 340 345 350
 Gly Val Ile Ala Met Thr Ser Ser Asp Ser Gln Ala Met Gly Arg Ala
 355 360 365
 Gly Glu Val Ile Pro Arg Thr Trp Gln Thr Ala Asp Lys Asn Lys Lys
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 Glu Phe Gly Lys Leu Pro Glu Asp Gly Ala Asp Asn Asp Asn Phe Arg
 385 390 395 400
 Ile Lys Arg Tyr Ile Ser Lys Tyr Thr Ile Asn Pro Ala Leu Thr His
 405 410 415
 Gly Val Ser Glu Tyr Ile Gly Ser Val Glu Glu Gly Lys Ile Ala Asp
 420 425 430
 Leu Val Val Trp Asn Pro Ala Phe Phe Gly Val Lys Pro Lys Ile Val
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 Ile Lys Gly Gly Met Val Val Phe Ser Glu Met Gly Asp Ser Asn Ala
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 Ser Val Pro Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met Phe Gly His
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 His Gly Lys Ala Lys Phe Asp Thr Ser Ile Thr Phe Val Ser Lys Val
 485 490 495
 Ala Tyr Glu Asn Gly Val Lys Glu Lys Leu Gly Leu Glu Arg Lys Val
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Leu Pro Val Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp Phe Lys Phe
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 Asn Asp Lys Thr Ala Lys Ile Thr Val Asp Pro Lys Thr Phe Glu Val
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